



DPPIV-5001-C1 PatentIn Replacement Sequence.ST25  
REPLACEMENT SEQUENCE LISTING

<110> Takeda San Diego, Inc.

<120> CRYSTALLIZATION OF DIPEPTIDYL PEPTIDASE IV (DPPIV)

<130> DPPIV-5001-C1

<140> 10/659,055

<141> 2003-09-09

<150> US 60/409,206

<151> 2002-09-09

<160> 3

<170> PatentIn version 3.3

<210> 1

<211> 766

<212> PRT

<213> Homo sapiens

<220>

<221> Amino acid sequence for full-length human wild type DPPIV

<222> (1)..(766)

<300>

<308> Genbank/NP\_001926

<309> 2002-02-19

<313> (1)..(766)

<400> 1

Met Lys Thr Pro Trp Lys Val Leu Leu Gly Leu Leu Gly Ala Ala Ala  
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Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr  
20 25 30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr  
35 40 45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser  
50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn  
65 70 75 80

Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp  
85 90 95

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln  
100 105 110

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Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr  
115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr  
130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val  
145 150 155 160

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile  
165 170 175

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp  
180 185 190

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Val Phe  
195 200 205

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala  
210 215 220

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe  
225 230 235 240

Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr  
245 250 255

Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn  
260 265 270

Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr  
275 280 285

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr  
290 295 300

Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln  
305 310 315 320

Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg  
325 330 335

Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly  
340 345 350

Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly  
355 360 365

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Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile  
370 375 380

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly  
385 390 395 400

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr  
405 410 415

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr  
420 425 430

Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu  
435 440 445

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu  
450 455 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr  
465 470 475 480

Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp  
485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys  
500 505 510

Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met  
515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu  
530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg  
545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala  
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His  
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu  
595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile  
610 615 620

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Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu  
625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val  
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly  
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val  
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His  
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser  
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr  
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr  
740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro  
755 760 765

<210> 2  
<211> 2184  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Human cDNA sequence encoding residues 39-766 of DPPIV  
<222> (1)..(2184)

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ttcaatgctg aatatggaaa cagctcagtt ttcttgaga acagtacatt tgatgagttt 180  
ggacattcta tcaatgatta ttcaatatct cctgatggc agtttattct cttagaatac 240  
aactacgtga agcaatggag gcattcctac acagcttcat atgacattta tgatttaat 300  
aaaaggcagc tgattacaga agagaggatt ccaaacaaca cacagtgggt cacatggtca 360  
ccagtgggtc ataaattggc atatgttgg aacaatgaca tttatgttaa aattgaacca 420

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gcaggagctg	tgaatccaac	tgtaaagttc	tttggtaa	atacagactc	tctcagctca	720
gtcaccaatg	caacttccat	acaaatca	gctcctgctt	ctatgttcat	aggggatcac	780
tacttgtgtg	atgtgacatg	ggcaacacaa	gaaagaattt	cttgcagtg	gctcaggagg	840
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tgcttagtgg	cacggcaaca	cattgaaatg	agtactactg	gctgggttgg	aagatttagg	960
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gaaggttaca	gacacatttgc	ctatttccaa	atagataaaaa	aagactgcac	atttattaca	1080
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tatacaaaag	tgacatgcct	cagttgtgag	ctgaatccgg	aaaggtgtca	gtactattct	1260
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ctctatactc	tacacagcag	cgtgaatgat	aaaggcgtga	gagtcctgga	agacaattca	1380
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aaatatcctc	tactattaga	tgtgtatgca	ggcccatgta	gtcaaaaagc	agacactgtc	1560
ttcagactga	actgggccac	ttaccttgca	agcacagaaa	acattatagt	agctagctt	1620
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gtggacaaca	aacgaattgc	aatttggggc	tggcatatg	gagggtacgt	aacctcaatg	1800
gtcctgggat	cgggaagtgg	cgtgttcaag	tgtggatag	ccgtggcgcc	tgtatccgg	1860
tgggagtact	atgactcagt	gtacacagaa	cgttacatgg	gtctcccaac	tccagaagac	1920
aaccttgacc	attacagaaa	ttcaacagtc	atgagcagag	ctgaaaattt	taaacaagtt	1980
gagtacctcc	ttattcatgg	aacagcagat	gataacgttc	actttcagca	gtcagctcag	2040
atctccaaag	ccctggtcga	tgttgagtg	gatttccagg	caatgtggta	tactgatgaa	2100
gaccatggaa	tagctagcag	cacagcacac	caacatata	atacccacat	gagccacttc	2160
ataaaaacaat	gtttctcttt	acct				2184

<210> 3  
<211> 740

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<212> PRT  
<213> Homo sapiens

<220>  
<221> N-terminal tag including a partial gp67 signal sequence and  
6x-histidine  
<222> (1)..(12)

<220>  
<221> Amino acid sequence for residues 39-766 of DPPIV with an  
N-terminal tag  
<222> (13)..(740)

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Tyr Thr Leu Thr Asp Tyr Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr  
20 25 30

Ser Leu Arg Trp Ile Ser Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn  
35 40 45

Asn Ile Leu Val Phe Asn Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu  
50 55 60

Glu Asn Ser Thr Phe Asp Glu Phe Gly His Ser Ile Asn Asp Tyr Ser  
65 70 75 80

Ile Ser Pro Asp Gly Gln Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys  
85 90 95

Gln Trp Arg His Ser Tyr Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn  
100 105 110

Lys Arg Gln Leu Ile Thr Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp  
115 120 125

Val Thr Trp Ser Pro Val Gly His Lys Leu Ala Tyr Val Trp Asn Asn  
130 135 140

Asp Ile Tyr Val Lys Ile Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr  
145 150 155 160

Trp Thr Gly Lys Glu Asp Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val  
165 170 175

Tyr Glu Glu Glu Val Phe Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro  
180 185 190

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Asn Gly Thr Phe Leu Ala Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro  
195 200 205

Leu Ile Glu Tyr Ser Phe Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys  
210 215 220

Thr Val Arg Val Pro Tyr Pro Lys Ala Gly Ala Val Asn Pro Thr Val  
225 230 235 240

Lys Phe Phe Val Val Asn Thr Asp Ser Leu Ser Ser Val Thr Asn Ala  
245 250 255

Thr Ser Ile Gln Ile Thr Ala Pro Ala Ser Met Leu Ile Gly Asp His  
260 265 270

Tyr Leu Cys Asp Val Thr Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln  
275 280 285

Trp Leu Arg Arg Ile Gln Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr  
290 295 300

Asp Glu Ser Ser Gly Arg Trp Asn Cys Leu Val Ala Arg Gln His Ile  
305 310 315 320

Glu Met Ser Thr Thr Gly Trp Val Gly Arg Phe Arg Pro Ser Glu Pro  
325 330 335

His Phe Thr Leu Asp Gly Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu  
340 345 350

Glu Gly Tyr Arg His Ile Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys  
355 360 365

Thr Phe Ile Thr Lys Gly Thr Trp Glu Val Ile Gly Ile Glu Ala Leu  
370 375 380

Thr Ser Asp Tyr Leu Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro  
385 390 395 400

Gly Gly Arg Asn Leu Tyr Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val  
405 410 415

Thr Cys Leu Ser Cys Glu Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser  
420 425 430

Val Ser Phe Ser Lys Glu Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly  
435 440 445

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Pro Gly Leu Pro Leu Tyr Thr Leu His Ser Ser Val Asn Asp Lys Gly  
450 455 460

Leu Arg Val Leu Glu Asp Asn Ser Ala Leu Asp Lys Met Leu Gln Asn  
465 470 475 480

Val Gln Met Pro Ser Lys Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr  
485 490 495

Lys Phe Trp Tyr Gln Met Ile Leu Pro Pro His Phe Asp Lys Ser Lys  
500 505 510

Lys Tyr Pro Leu Leu Leu Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys  
515 520 525

Ala Asp Thr Val Phe Arg Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr  
530 535 540

Glu Asn Ile Ile Val Ala Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln  
545 550 555 560

Gly Asp Lys Ile Met His Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu  
565 570 575

Val Glu Asp Gln Ile Glu Ala Ala Arg Gln Phe Ser Lys Met Gly Phe  
580 585 590

Val Asp Asn Lys Arg Ile Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr  
595 600 605

Val Thr Ser Met Val Leu Gly Ser Gly Ser Gly Val Phe Lys Cys Gly  
610 615 620

Ile Ala Val Ala Pro Val Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr  
625 630 635 640

Thr Glu Arg Tyr Met Gly Leu Pro Thr Pro Glu Asp Asn Leu Asp His  
645 650 655

Tyr Arg Asn Ser Thr Val Met Ser Arg Ala Glu Asn Phe Lys Gln Val  
660 665 670

Glu Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn Val His Phe Gln  
675 680 685

Gln Ser Ala Gln Ile Ser Lys Ala Leu Val Asp Val Gly Val Asp Phe  
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695 700

Gln Ala Met Trp Tyr Thr Asp Glu Asp His Gly Ile Ala Ser Ser Thr  
705 710 715 720

Ala His Gln His Ile Tyr Thr His Met Ser His Phe Ile Lys Gln Cys  
725 730 735

Phe Ser Leu Pro  
740